

GGGCTAGGG CGCCGGGTCA GGGGCTCGA GATCGGGCTT GGGCCAGAG C ATG TTC 57  
 Met Phe  
 1

CAG ATC CCA GAG TTT GAG CCG AGT GAG CAG GAA GAC TCC AGC TCT GCA 105  
 Gln Ile Pro Glu Phe Glu Pro Ser Glu Gln Glu Asp Ser Ser Ser Ala  
 5 10 15

GAG AGG GGC CTG GGC CCC AGC CCC GCA GGG GAC GGG CCC TCA GGC TCC 153  
 Glu Arg Gly Leu Gly Pro Ser Pro Ala Gly Asp Gly Pro Ser Gly Ser  
 20 25 30

GGC AAG CAT CAT CGC CAG GCC CCA GGC CTC CTG TGG GAC GCC AGT CAC 201  
 Gly Lys His His Arg Gln Ala Pro Gly Leu Leu Trp Asp Ala Ser His  
 35 40 45 50

CAG CAG GAG CAG CCA ACC AGC AGC AGC CAT CAT GGA GGC GCT GGG GCT 249  
 Gln Gln Glu Gln Pro Thr Ser Ser Ser His His Gly Gly Ala Gly Ala  
 55 60 65

GTG GAG ATC CGG AGT CGC CAC AGC TCC TAC CCC GCG GGG ACG GAG GAC 297  
 Val Glu Ile Arg Ser Arg His Ser Ser Tyr Pro Ala Gly Thr Glu Asp  
 70 75 80

GAC GAA GGG ATG GGG GAG GAG CCC AGC CCC TTT CGG GGC CGC TCG CGC 345  
 Asp Glu Gly Met Gly Glu Glu Pro Ser Pro Phe Arg Gly Arg Ser Arg  
 85 90 95

TCG GCG CCC CCC AAC CTC TGG GCA GCA CAG CGC TAT GGC CGC GAG CTC 393  
 Ser Ala Pro Pro Asn Leu Trp Ala Ala Gln Arg Tyr Gly Arg Glu Leu  
 100 105 110

CGG AGG ATG AGT GAC GAG TTT GTG GAC TCC TTT AAG AAG GGA CTT CCT 441  
 Arg Arg Met Ser Asp Glu Phe Val Asp Ser Phe Lys Lys Gly Leu Pro  
 115 120 125 130

CGC CCG AAG AGC GCG GGC ACA GCA ACG CAG ATG CGG CAA AGC TCC AGC 489  
 Arg Pro Lys Ser Ala Gly Thr Ala Thr Gln Met Arg Gln Ser Ser Ser  
 135 140 145

TGG ACG CGA GTC TTC CAG TCC TGG TGG GAT CGG AAC TTG GGC AGG GGA 537  
 Trp Thr Arg Val Phe Gln Ser Trp Trp Asp Arg Asn Leu Gly Arg Gly  
 150 155 160

Fig. 1A

0922378-080301

AGC TCC GCC CCC TCC CAG TGACCTTCGG TCCACATCCC GAAATCCACC 585  
Ser Ser Ala Pro Ser Gln  
165

CGTTCCTTATT GCCCTGGGCA GCCATTTTGA ATATGGGAGG AAGTAAGTTC CCTCAGGCCT 645

ATGCAAAAAG AGGATCCGTG CTGTATCCTT TGGAGGGAGG GTTGACCCAG ATTCCCTTCC 705

GGTGTGTGTG AAGCCACGGA AGGTTGGTCC CATCGGAAGT TTTGGGTTTT CCGCCCACAG 765

CCGCCGGAAG TGGCTCCGTG GCGCCGCCCT CAGGTTCCGG GGTTCCTCCC AGGCGCCTGC 825

GCTAAGTAGC GAGCCAGGTT TAACCGTTGT GTCACCGGGA CCGAGCCCC CGCGATGCCC 885

TGGGGGCCGT GATCAGTACC AAATGTTAAT AAAGCCCGCG TGTGTGCCAA AAAAAAAAAA 945

A 946

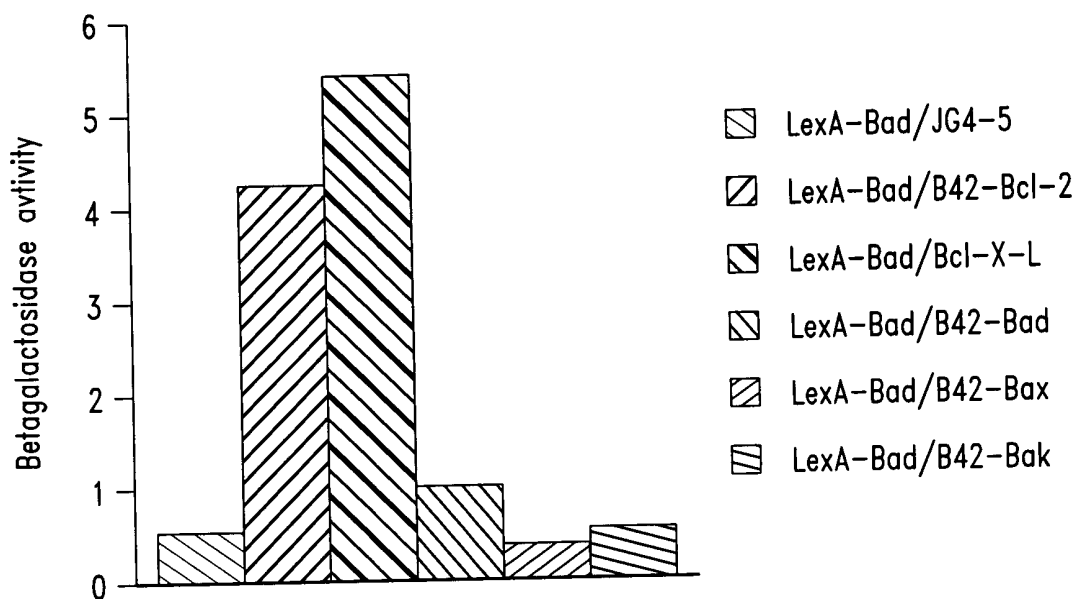
*Fig. 1B*

0922378.080304

10 20 30 40  
 1 M G T P K Q P S L A P A H A L G L R K S D P G I R S L G S D A G G R R W R P A A PmBad  
 1 - - - - - PBM1  
 50 60 70 80  
 41 Q S M F Q I P E F E P S E Q E D A S A T D R G L G P S L T E D Q P G P Y - - - PmBad  
 1 - - M F Q I P E F E P S E Q E D S S S A E R G L G P S P A G D G P S G S G K H H PBM1  
 90 100 110 120  
 77 - L A P G L L G S N I H Q Q G R A A T N S H H G G A G A M E T R S R H S S Y P A PmBad  
 39 R Q A P G L L W D A S H Q Q E Q P T S S S H H G G A G A V E I R S R H S S Y P A PBM1  
 130 140 150 160  
 116 G T E E D E G M E E E L S P F R G R S R S A P P N L W A A Q R Y G R E L R R M T PmBad  
 79 G T E D D E G M G E E P S P F R G R S R S A P P N L W A A Q R Y G R E L R R M S PBM1  
 170 180 190 200  
 156 D E F E G S F K - G L P R P K S A G T A T Q M R Q S A G W T R I I Q S W W D R N PmBad  
 119 D E F V D S F K K G L P R P K S A G T A T Q M R Q S S S W T R V F Q S W W D R N PBM1  
 210  
 195 L G K G G S T P S Q PmBad  
 159 L G R G S S A P S Q PBM1

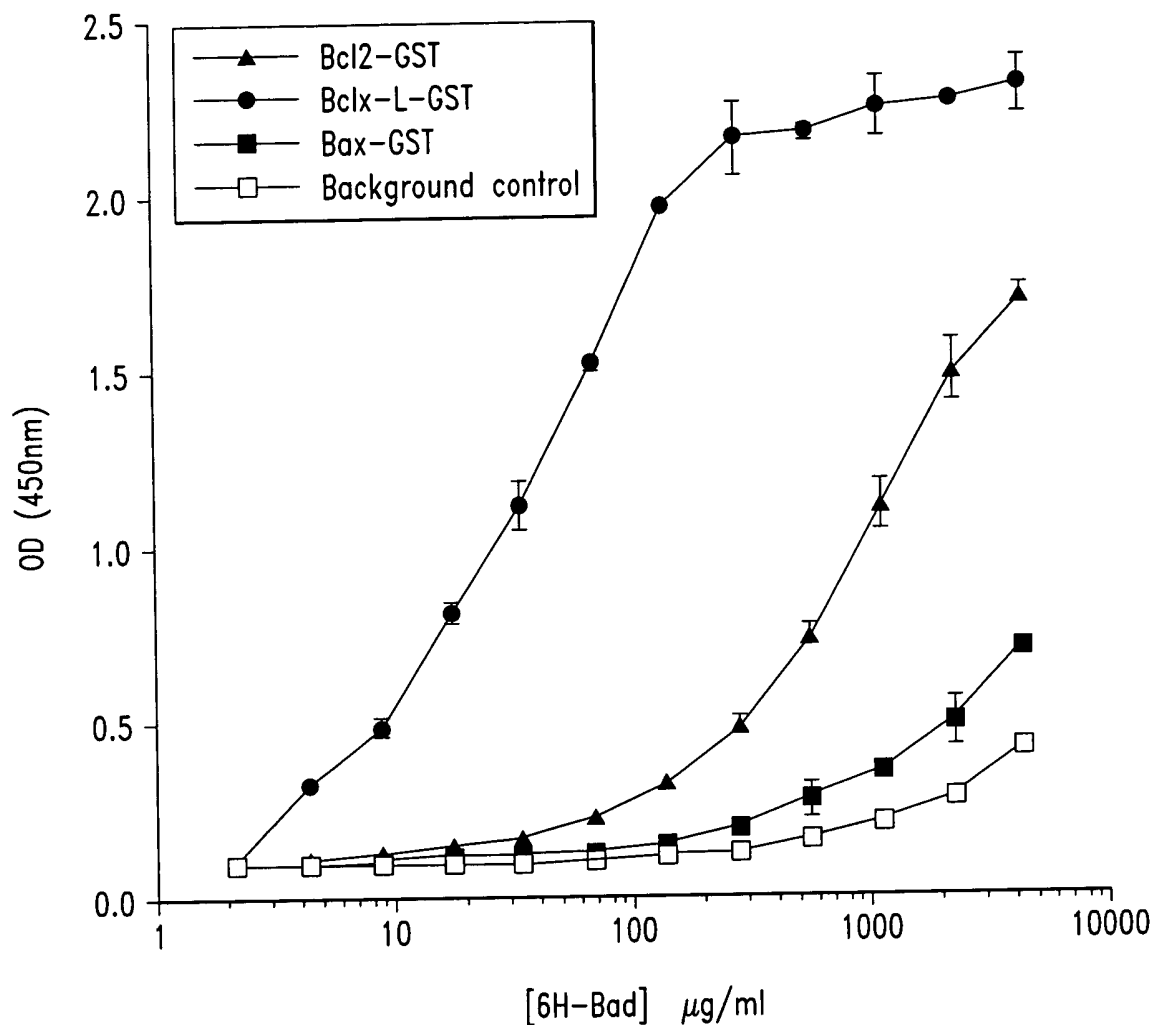
*Fig. 2*

### Bad 2-Hybrid Interactions



*Fig. 3*

## Binding of Bcl-2 Family Proteins to Bad



*Fig. 4*